

Abstract

The tea industry is significant in the economies of tea-growing countries. Prospects of improving yield of made tea genomic information were explored using clones from a cross between clones TRFCA SFS150 and AHP S15/10. The 42 clones were tested in two distinct tea-growing regions in Kenya. Bulk segregant analysis was performed followed by complete genotyping. Out of 260 informative markers, 100 markers that showed 1:1 segregation were used to construct a linkage map. The map contained 30 (19 maternal and 11 paternal) linkage groups that spanned 1,411.5 cM with mean interval of 14.1 cM between loci. Based on the map, quantitative trait loci (QTL) analysis was done on yield data over 2003 – 2007 across the two sites, Timbilil and Kangaita. Twenty-three putative QTLs were detected, 16 in five different linkage groups for Timbilil, two in two groups for Kangaita, and the rest were associated with unassigned markers. No QTL was detected at both sites, which showed strong genotype×site interaction ($G \times E$) but highly effective within-site heritability (h^2 generally > 0.7). Problems of overestimated and spurious QTL effects arising from the smallness of the population should be mitigated by generally high within-site heritability. At least two unassigned markers associated with yield at Kangaita over the whole study period, suggesting potential as candidate markers for site-specific marker-assisted selections. Implications of the results with respect to mapping population, $G \times E$, and marker-assisted selection are discussed.